

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1393	42.6	689	1	JW0107	very-long-chain ac
2	1044	31.9	646	1	A55093	fatty acid transpo
3	958	29.3	650	2	T21498	hypothetical prote
4	953	29.1	608	2	H83284	probable very-long
5	944	28.9	597	2	D70609	probable fadB6 pro
6	936	28.6	655	2	T15879	hypothetical prote
7	913.5	27.9	643	2	T43052	fatty acid transpo
8	744.5	22.8	623	2	S45899	probable membrane
9	398.5	12.2	502	2	D70806	probable fadB17 pr
10	398.5	12.2	522	2	S40586	probable carnitine
11	397.5	12.2	522	2	H85484	probable crotonobe
12	387.5	11.8	999	2	B70501	hypothetical prote
13	385	11.8	532	2	G70986	probable coA ligas
14	354.5	10.8	513	2	A69331	probable acid--CoA
15	335	10.2	569	2	D82834	regulator of patho
16	334	10.2	569	2	C69471	probable fatty-aci
17	332.5	10.2	521	2	F84288	hypothetical prote
18	332.5	10.2	554	2	A70904	probable acid--CoA
19	332.5	10.2	593	2	E69378	probable acid--CoA
20	331.5	10.1	560	2	A70628	probable acid--CoA
21	329	10.1	503	2	E70523	probable acid--CoA
22	314	9.6	444	4	T50931	probable acid--CoA
23	312.5	9.6	549	2	G69335	hypothetical prote
24	306.5	9.4	552	2	E69438	probable acid--CoA
25	302.5	9.2	566	2	H84037	probable fatty-aci
26	299.5	9.2	565	2	T16318	long-chain fatty-a
27	299	9.1	549	2	F69093	hypothetical prote
28	297.5	9.1	599	2	H72454	probable acid--CoA
29	297.5	9.1	632	2	B83161	probable fatty-aci
						probable AMP-bind1

Db 422 FGPDIRWEYFGSTEGNVLNMYVGHGAGVTRSCILRLMTPPELYQFDIETAEPLRQK 481  
QY 413 YCVRPKGEVGLLVCKITQITLPNGYAGAKAOTEKKLRDVKFKGDLNFNSGDLMDVDE 472  
Db 482 FCIPVPGKPGLLTKVRKNQPFGLYRGSGAESNRKLVANVRVGLDYFNTGDLVTLQDE 541  
QY 473 NFYIFHDRVGDTRFKWGENVATEVADTVGLVDFVQEVNMYGVHVPDHEGRIGMASIKMK 532  
Db 542 GFFYQDRLGDTFRWKGENVTEGEVSLSSLDLEEVNMYGVPPVCGEKGKMAVAKLA 601  
QY 533 ENHEFGKLFQHIADYLPSPARFRLQDTIETITGTFKHKRMTLVEEFGFPAVVKDAL 592  
Db 602 PGKTFDQKLYQHVRSWLPAYATPHFIRIQDSLEITNTYKLVKSRLVREGFDVGIADPL 661  
QY 593 YFLDDTAKMYVMTEDIYNAISAKTLK 620  
Db 662 YILDNAQOTFRSLMPDQVYQAVCEGTWKL 689

## RESULT 2

A55093  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Sep-2000  
C:Accession: A55093; 149132  
R:Schaffer, J.E.; Lodish, H.F.  
Cell 79, 427-436, 1994  
A:Title: Expression cloning and characterization of a novel adipocyte long chain fatty acid  
A:Reference number: A55093; MUID:95042740  
A:Accession: A55093  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-646 <SCH>  
A:Cross-references: GB:U15976; NID:9563828; PIDN:AACT1060.1; PID:9563829  
A:Gene: FATP  
C:Genetics:  
A:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase h  
F;124-604/Domain: acetate--CoA ligase homology <ACL>

Query Match 31.9%; Score 1044; DB 1; Length 646;  
Best Local Similarity 40.0%; Pred. No. 7.6e-73;  
Matches 247; Conservative 83; Mismatches 245; Indels 42; Gaps 11;  
QY 33 FLKVAAGVRVRVSG-----QRRPARTILRAFLERAKOTPHKPFLLFRDETL 79  
Db 43 FLRIVCKTARRDLGLSVLRVLRLELRHRRAGDTIPCFQAVARQPERALVLDASSGI 102  
QY 80 --TYAQVDRSNQVARNALHDHGLRGDCVALLMGNEPAYVWLWGLVKLGCMACLNYN 137  
Db 103 CWTFAQLDTSNAYAN-LFRQLGFAPGDVAVFLEGRPEFVGLWGLAKAGVVAALLN 161  
QY 138 IRAKSLHLCQCCGAKVLLVSPLEQAAVEILPSLKKDDVSIYVSKTSNTDGDIDFLDK 197  
Db 162 LRREPLAFCLGTSNAKALITGGEMAAVAEVSQLGKS-----LLKFCSDGLGPESILPD 216  
QY 198 VD-----EVSTPEI---PESRSEVTFSTPALYITSTGTLGLPKAAMTHQRIWYGTG 247  
Db 217 TQLDPLALAEAPTTPLAQAPGKMDRLF-----YIYTSCTGLPKAAIVHVSRYRIA 271  
QY 248 LTFVS-GLKADDVYIITLPYHSAALLIGHCIVAGATLALTKFSASQFDDCRKYNV 306  
Db 272 FGHSYSMAADVLYDCLPLYHSAAGNMGVQCIVYGLTVVLRKFSASRFDDCKYK 331  
QY 307 TVIYIGELRLYCNLPQKNDNRDHKVRALGNLGRDVRQVRFKRGDICIYEFYAATE 366  
Db 332 TVVYIYIGELRYLLRQVDRVQEHVRLAVGNLRAIPAIWEEFTQREGVPIGEFYGATE 391  
QY 367 GNIGFMNARKVAGVGNVYVQKLIYDLYKVDVEKDEPVRDENGVCYVRVPGEGVLLV 426  
Db 392 CNCSTIANMDGKVGCGFNSRLTHVYPIRLVKVNEEDTMEPLRDESEGLICPCQGEPLV 451  
QY 427 CKITQLTP---FNGYAGAKAOTEKKLRDVKFKGDLVFNNSGDLMDVDEHNFYFHDRVGD 483

Db 452 GOINQOPLRRFDGYVSDSA-TNKKIAHSVFRKSDSAYLSGDVLMDELGYMYFRDRSGD 510  
QY 484 TFRWKGENVATEVADTVGLVDFVQEVNMYGVHVPDHEGRIGMASIKMKENHEFDEKFLP 543  
Db 511 TFRWKGENVSTTEVEAVLSRLLGQTDVAVYGVAVPGVEGKAGMAAI-ADPHSOLDPNSMY 569  
QY 544 OHIADYLPSPARFRLQDTIETITGTFKHKRMTLVEEFGFPAVVKDALYFLDDTAKMYV 603  
Db 570 QELQKVLASARPIFLRLPOVDTTGFKIQKRLQREGFDPRQTSRDLFFLDLKQGRYV 629  
QY 604 PMTEIDIYNAISAKTLK 620  
Db 630 PLDERVHARICAGDFSL 646

## RESULT 3

T21498  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 02-Sep-2000  
C:Accession: T21498  
R:Baynes, C.  
submitted to the EMBL Data Library, April 1996  
A:Reference number: Z19430  
A:Accession: T21498  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-650 <WTL>  
A:Cross-references: EMBL:Z70684; PIDN:CRA94602.1; GSPDB:GN00022; CESP:F28D1.9  
A:Experimental source: clone F28D1  
C:Genetics:  
A:Gene: CESP:F28D1.9  
A:Map position: 4  
A:Introns: 55/2; 87/2; 120/3; 187/1; 241/1; 356/1; 395/1; 600/1  
C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase  
F;123-609/Domain: acetate--CoA ligase homology <ACL>

Query Match 29.3%; Score 958; DB 2; Length 650;  
Best Local Similarity 38.5%; Pred. No. 3.5e-66;  
Matches 222; Conservative 97; Mismatches 225; Indels 32; Gaps 15;  
QY 59 FLEKARQTHPKPFL--LFRDETLTYAQVDRSNQVARNALHDHGLRGDCVALLMGNEPA 116  
Db 81 FLDIVYKKNPKAMIDTETNTTETAYEAFNHCNRYANYFOG-LGYRSGDVVVALTWNSVE 139  
QY 117 YVWLWGLVGLKGCAMACLNYNIRAKSLHLCQCCGAKVLLVSPLEQ-----AAVEEILPSL 172  
Db 140 FVAAMWGLAKGVYTAWLNLSNLRQLVHCITASKTRAITSVTLQNLMLDAIDQKL--F 197  
QY 173 KDDVSIYVSKTSNTDGDIDSLDKVD-EVSTPEIPESRSEVTFSTPALYIYTSGTGL 231  
Db 198 DVEGIEVYSGEPKKNKSGFKLKKLDAQITTEP---KTLDIVDFKSLCFIYTSGTGM 254  
QY 232 PKAAMITHQ---IWKYGLTFVSLKADDVYIITLPYHSAALLIGHCIVAGATLAL 288  
Db 255 PKAAWKKHFRYYSIAVGAAKSF--GIRPSDRMYSMPIYHFAAGILGVQALLGGSCVI 312  
QY 289 RTKFSASQFDDCRKYNVTIYIGELRLYCNLPQKNDNRDHKVRALGNLGRDVRQ 348  
Db 313 RKKFSASNFWRDVKYDCTVSQYIGEICRYLLAQPVVEESRHRMLRVGLNGLRAEIWQP 372  
QY 349 FVKRGDICIYEFYAATEGNIGFMNARKVAGV--RVNYLQKKLIYDLYKDYVERDEP 406  
Db 373 FVDRF-RVRIGELYSTEGTSLNVNIDHVGACGFLPSITPKMHVRLRLKVDVDTGEA 431  
QY 407 VRDENGVCYVRVKGEGVGLLVCKITQTP---FNGYAGAKAOTEKKLRDVKFKGDLVFN 463  
Db 432 ITSDGLCIACNPGSGAMVSTIRKNNLLOFEGYLN-KKETNKKIIRDFVAKGSCFLT 490  
QY 464 GDLLMVDHNFYFHDRVGDTRFKWGENVATEVADTVGLVDFVQEVNMYGVHVPDHEGR 523



Db 566 DPLYVLAPDEGYVP 580

## RESULT 6

T15879  
hypothetical protein D1009.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 02-Sep-2000  
C:Accession: T15879  
R:Favella, T.  
A:Description: The sequence of C. elegans cosmid D1009.  
A:Reference number: Z18422  
A:Accession: T15879  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-655 <FAV>  
A:Cross-references: EMBL:U40938; NID:g1072169; PID:g1072173; PIDN:AAA81698.1; CESP:D1009  
C:Gene: CESP:D1009.1  
A:Introns: 2/2; 60/2; 89/3; 125/3; 192/1; 344/2; 399/1; 547/3; 569/3; 602/1  
C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase  
F:128-611/Domain: acetate--CoA ligase homology <ACL>

Query Match 28.6%; Score 936; DB 2; Length 655;  
Best Local Similarity 36.9%; Pred. No. 1.8e-64;  
Matches 244; Conservative 95; Mismatches 245; Indels 78; Gaps 19;

QY 6 YTVLAGLLFLPLVNLCCPYF-PQDIGYFLKVAAGRRVRS-YGQRRPA-----52  
Db 10 FALVTFTVAVLVYNSVFWKVFYIG-----VFRLLRTDFGRALATLPRDFAGLKL 64  
QY 53 -----RTILRAFLKARQTPHPKFLFRD--ETLTVQVDRRSNOVARAL 95  
Db 65 LISVKSTIRGLFKKDRPIHEIFLNQVQHPNKVAIIIESGRLIYQELNALANQYAN-L 123  
QY 96 HDHLGRQDCVALLMGNEPAYVWLGLVKGCMACNLNIRAKSLHLCFCQCGAKVL 155  
Db 124 YVSEGYKMGDVALFENSIDFPAIWLGLSKIGVSAFNSNKLPLELAHSINVSKCKSC 183  
QY 156 LVS-----PELQAAVEELPSLKDDVSIYVSVTSNTDG-----IDSFLDKVDVSTEP 205  
Db 184 ITINILNLPFKAAREK---NLISDEIHLVFLAG--TVQDGRHSLOQDLHLFSEDE---PP 235  
QY 206 IPESWRSEVTFSTPALYITSTGTLGPKAAMITHOR-IMYGTGLTFVSGLKADDVYITL 264  
Db 236 VIDG-----LNFERSVLCYITSTGTPGNPKPAVIKHERYFWIAGAGKAFGINKSDVYITM 291  
QY 265 PFYHSAALLIGHCIVAGATLALRTKFSASQFWDRCRKYNTVIQYIGELLRYLCSNQ 324  
Db 292 PMYHSAAGIMGSLIAFGSTAVIRKFSASNFWDCKVKNYATQYIGEICRYLLAAMP 351  
QY 325 KPNDRDHKVRLALGNLGRDVRQFVKRFGDICIYEFYAATEGNIGFMNRYARKVGAAGRV 384  
Db 352 CPEKQHNVRMLMGNGLRGQIWEFVGRGKIGKIGELYSTEGNSINVINVDNHVGCAGFM 411  
QY 385 NYLQK---KIITYDLIKYDVEKDEPRDENGVCYVRPKGEVGLLVCKITQ---LTPNGYA 439  
Db 412 PIVPHIGSLYPRLLIKVDRTAGELERDKNGLCVPCVPGETGEMGVYKEKIDILLKEGYV 471  
QY 440 GAKAQTEKKLRLRVFKGDLFYNSGDLVVDHENFIYFHDRVGDTPFRWGENVATEVAD 499  
Db 472 -SEGDTAKTKIYRDFVHGDKVFASGDLHWDLDLGYLYFVDRCGDTPFRWGENVSTTEVG 530  
QY 500 TVGLVDPRQVBNVYGVHVPDHEGRIGMASIKMKENHEFGGKLFQIADY-----LPS 552  
Db 531 ILQPMVDVEDATYGVTVGKMEGRAGMAGIVVK-----DGTDEKEFIADITSLETNLAS 585  
QY 553 YARPRFLRIQDTITGTFKHKMTLVEEGFNPAVTK-DALYFLDDTAKMYVPMTEDIYN 611  
Db 586 YAIPIVTRICKVEDTGTGTFKLLKTDLQKQGYDLVACKGDPYIYWSAAEKSYKPLTDKMQQ 645

QY 612 AI 613  
Db 646 DI 647

## RESULT 7

T43052  
fatty acid transport protein - fungus (Cochliobolus heterostrophus)  
C:Species: Cochliobolus heterostrophus, Bipolaris maydis  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 02-Sep-2000  
C:Accession: T43052  
R:Oesser, B.M.  
A:Title: PKC1, encoding a protein kinase C, and FAT1, encoding a fatty acid transport  
A:Reference number: 222303; MUID:98415124  
A:Accession: T43052  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-643 <OES>  
A:Cross-references: EMBL:Y15839; NID:g2687848; PIDN:CAA75802.1; PID:g2687850  
A:Experimental source: strain C2 (ATCC 48329)  
C:Genetics:  
A:Gene: fat1  
A:Introns: 169/3; 478/2  
C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase  
F:121-599/Domain: acetate--CoA ligase homology <ACL>

Query Match 27.9%; Score 913.5; DB 2; Length 643;  
Best Local Similarity 34.9%; Pred. No. 9.8e-63;  
Matches 210; Conservative 112; Mismatches 238; Indels 41; Gaps 12;

QY 39 VGRVRSYVGRRPARTIL--RAFLKARQTPHPKFLFRDLETLYAQVDRRSNOVARALH 96  
Db 65 INRRV---AOKR-----VLTHHIFQEQVQKOSNHPFLFEKGTWSYKEFSAYTRVNWLI 117  
QY 97 DHGLGRQDCVALLMGNEPAYVWLGLVKGCMACNLNIRAKSLHLCFCQCGAKVL 156  
Db 118 DELDQVGMVAIDGGSAEHLMLWALDAIGAATSFNLWNLGTAGLHICKECFRVI 177  
QY 157 VSPLEQAAVEELPSLKDDVSIYVSVTSNTDGIDSLDKVDVSTEPPEPESWRSEVTF 216  
Db 178 ADIDIKANIEPCRGEELETGINIHYD-----PSFISSLP--NNTPIDSRSTENIEL 227  
QY 217 STPALYITSTGTLGPKAAMI-THQRIWYGTGLTFVSGLKADDVYITLPHYSAALLIG 275  
Db 228 DSVRGLIYTSGTGLPKGVFISTGRELRTDWSISKYLNLPKPTDRMYTCMPLYHAAHSLC 287  
QY 276 IHGCIIVAGATLALRTKFSASQFWDRCRKYNTVIQYIGELLRYLCSNQPNDRDHKVR 335  
Db 288 TASVTHGGGTVVLSEKTSKHKFWFPEVVAEANIIOYVGLGRYLLNGPKSPYDRAHKVQ 347  
QY 336 ALGNLGRDVMRQVVRKFGDICIYEFYAATEGNIGFM-----NYARKVGAVGRVN 385  
Db 348 AWNGMRPDVWEAFREFRNIPILHELYAATDG-LGSMTRNAGPPTANCIALRLGIHWK 406  
QY 386 YLQKIIITYDLIKYDVEKDEPRDENGVCYVRPKGEVGLLVCKIT--QLTPFNGYAGAKA 443  
Db 407 FRNOEV-----LVKMDLDTDEIMDRNGFAIRCAVNEPQMLFRTPETLAGAPSYNNET 462  
QY 444 QTEKKLRDVPFKGDLVFNSGDLLMVDHENFIYFHDRVGDTPFRWGENVATEVADTVGL 503  
Db 463 ATQSRITDVFQKGLDLPKSGDMLRQDAEGRVYFVDRDGTFRWKSENVSTNEVADVMGT 522  
QY 504 VDFQVQVNVYGVHVPDHEGRIGMASIKMKENHEFGGK--KLFOHIADYLPFSYARPRELRI 561  
Db 523 FPQIAETNVYGLVPGNDGRVRSNCHRRDRDVRDIFRAALAKHARDRLPGYAVPLEFLRV 582  
QY 562 QDTTEITGTFKHKMTLVEEGFNPAVI--KDALYFLDDTAKMYVPMTEDIYNALSATLK 619  
Db 583 TPALYETGTLKIQGRKQEGIDPKTSGEDKLYWLPGPSDIYLPFGKMEQGVLDKRIIR 642  
QY 620 L 620

Db 643 L 643

## RESULT 8

S45899

probable membrane protein YBR041w - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein YBR0411

C;Species: Saccharomyces cerevisiae

C;Date: 26-Aug-1994 #sequence\_revision 09-Sep-1994 #text\_change 02-Sep-2000

C;Accession: S45899

R;Andre, B.; Cziepluch, C.; Hein, C.; Jauniaux, J.C.; Urrestarazu, A.; Vissers, S.

submitted to the Protein Sequence Database, August 1994

A;Reference number: S45899

A;Accession: S45899

A;Molecule type: DNA

A;Residues: 1-623 &lt;AND&gt;

A;Cross-references: EMBL:Z35910; NID:G536263; PIDN:CAA84983.1; PID:G536264; MIPS:YBR041w

A;Experimental source: strain S288C

C;Genetics:

A;Gene: SGD:PAT1

A;Cross-references: SGD:S0000245; MIPS:YBR041w

A;Map position: 2R

C;Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase bc

C;Keywords: transmembrane protein

F;1-27/Domain: transmembrane #status predicted &lt;TM1&gt;

F;55-71/Domain: transmembrane #status predicted &lt;TM2&gt;

F;133-623/Domain: acetate--CoA ligase homology &lt;ACL&gt;

F;149-167/Domain: transmembrane #status predicted &lt;TM3&gt;

F;304-322/Domain: transmembrane #status predicted &lt;TM4&gt;

## Query Match

Best Local Similarity 22.8%; Score 744.5; DB 2; Length 623;

Matches 191; Conservative 96; Mismatches 236; Indels 59; Gaps 16;

QY 24 PYFFDIDGVLKVAAGR-----RVRSYQRRPARTILRAFLKARQTPHPKPF 72

Db 58 PYFLKSV--FCYIIDVRRHFQNWYLFKIQVQNGDHL-AISYTRPMAEKG----- 106

QY 73 LPRDELTVAQVDRRSNOVARALHDHGLRGDCVALLMGNEPAYVWLGLVGLGAMA 132

Db 107 -POLTEFFYIETYNVLKSLHILHFDYNVQAGDYVAIDCTNKLPLFVLWLSLWNGAIPA 165

QY 133 CLNYYNIRAKSLHLCQCCGKAVLLVSPQLAAVEILPSLKK--DVSYYVVSRTSNTDG 190

Db 166 FLNYYTKGTPLVHLSKINISITQVFDPPASNPIRESEEEIKNALPDVKNLYLEQ----- 220

QY 191 IDSFLDKYDEVSTPIPESEWSE-----VTFSTPALYIYTSGLPKAAMTHORIW 243

Db 221 -----DLMHLLNSQSPFLOQDNVTRPLGLTDFKPSMLIYTSGLPKSAIMSWRKSS 275

QY 244 YGTGL-TEVSGLKADDVYIITLPFYHSAALLIGHGICVAGATLALRTKFSASQFWD 302

Db 276 VGCQVEGHVLMHNTSTVFTAMPLFHSYTAALLGACAILSHGGCLALSHKFSASTFWQVY 335

QY 303 KYNVTIYQIGELLRLYCNPSQKPNDRDHKVRALGNLGRDVMRQVFRFGDICIYEFY 362

Db 336 LTGATHIQYGVGEVCRYLLHTPISKYEMHKVKVAYGNGLRPDIWQDFRKRNFIEVEFY 395

QY 363 AATEGNIGFMNAR---KVGAVGRVNYLOKKIITYD--LKYDEKDEPV-RDENGVCVR 416

Db 396 AATEAPATTTTQKDGFGIGACRNYGTIIQWFLSQOTLVRMDPNDDSVIYRNSKGCEV 455

QY 417 VPKGEVGLLVCKI-----TQTFPFNGYAGAKAQTCKKLRDVKFKGDLFYNSGDLMLVDHE 472

Db 456 APVGEPMGLMRIFPPKPKPESFGYLGNAKETKSKVVRDVRFGDANYRCGDLMLKADEY 515

QY 473 NFIFYHEDVGTTFRWKGENVATTEVAD--TVGLVDFVQENVYGVHVPDHEGRIGMASIK 530

Db 516 GLWYFLDRMGDTFRWKSSENSTTEVEDQLTASNKEQYQVLLVGVGKVPKVEGRAGAVIK 575

QY 531 MKENH-EFDGK-KLFOHIAD--YLPYSVRPRFLRIQDTIET 568

Db 576 LTDNSLDITAKTKLNDLSRLNLPSPYAMPFLVFKFVDEIKMT 617

## RESULT 9

D70806

probable fadD17 protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 18-Aug-2000

C;Accession: D70806

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A;Reference number: A70500; MUID:98295987

A;Accession: D70806

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-502 &lt;COL&gt;

A;Cross-references: GB:AL022022; GB:AL123456; NID:G3261554; PIDN:CAA17743.1; PID:G292

A;Experimental source: strain H37Rv

C;Genetics:

A;Gene: fadD17

C;Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology

F;51-486/Domain: acetate--CoA ligase homology &lt;ACL&gt;

## Query Match

Best Local Similarity 12.2%; Score 398.5; DB 2; Length 502;

Matches 149; Conservative 78; Mismatches 218; Indels 85; Gaps 20;

QY 74 FRETLYTAQVDRRSNOVARALHDHGLRGDCVALLMGNEPAYVWLGLVGLKLG 128

Db 25 FEDSFTSWDRHRIHGAIAAALRERLDPPRPPHGVLLQNTFFSATLVAGALSGIVPVG 84

QY 129 CAMACLYNTRAKSLHLCFCOCGKAVLLV---SPELQAAVEEILPSLKKDDVSIYVSR 185

Db 85 -----LNPVRGGAALAGADIAKDCQLVLTGSGSAEVPADVEHI----- 122

QY 186 SNTDGDIDSLDKYDEVSTPIPESEWSEVTFSTPAL-----YIYTSGLPKAAMTHQ 240

Db 123 ----NVDSP-PEWTEVAAHR-----DTEVFRSADLADLFMLIFTSGDPRKAVKCSHR 172

QY 241 RIWY-GTGLTFVSGLKADDVYIITLPFYHSAALLIGHGICVAGATLALRTKFSASQFWD 299

Db 173 KVAIAGVTITQRFSLGRDDVCYVSMPLFHSNVLVGVMAVAAACQGSMAWLRKFSASQFLA 232

QY 300 DCRKYNVTIYQIGELLRLYCNPSQKPNDRDHKVRALGN-GLRGDVMRQVFRFGDICI 358

Db 233 DVRYGATYANVVKPLSVLATPELPDNDNPLRAVYGNVGVPGDIDR-FGRREGCV-V 290

QY 359 YEFYAATEGNIGF-MNARKVGAAGRVNYLOKKIITYDLIKYDVEKDEPVRDENGVCVRV 417

Db 291 MDGFGSTEGVATITRLDTPAGALGP-----LPGGIQIVDPDTEP-----C 332

QY 418 PRKEVGLLVCKITQLTP--FNGYAGAKAQTCKKLRDVKFKGDLFYNSGDLMLVDHENFI 475

Db 333 PTGVVGLV---NTAGPGGEGYINDEAAEAERMAAGV-----YHSGDLAYRDDAGYA 382

QY 476 YFHDRVGDTRFRKGENVATTEVADTVGLVDFVQENVYGVHVPDHEGRIGMASIKKENH 535

Db 383 YFAGRLGDMMVRDGENLGTAPITVRLMRYPDATVAVYVPPDVPVQDQV-MAAVLAPGT 441

QY 536 EFDGKLFQHIADYLPYSAR---PRFLRIQDTIETITGTFKHKRMTLVEEG 582

Db 442 KFDADK-FRAFLTEQPDLGHKQWPSVVRVYAGLPRMTTFKVIKROLSAEG 490

## RESULT 10

S40558

probable carnitine--CoA ligase (EC 6.2.1.-) - Escherichia coli

Qy	80	TYAQVDRRSNOVARALHDHJGLRGQSCVALLMGNEPAYVWMLGVLKVGCMACLNYNIR	139
	:	: : : :	:
Db	44	SYLENGEINRTANLEFT-JGIRKGGBLHLDNCPFEFICFWFLGAKIGAIMVPINARLL	102
	:	: : : :	:
Qy	140	AKSILLHCFOCCGAKVILLVSPELQAAVEETILPSLKDKDVSIYXVSRTS-----NTDGDISFL	195
	:	: : : :	:
Db	103	CEESAWILQNSQACRLVTYSAQFPYMQOI---QEEDATQLRHCLITDVALPADDGVSSFT	159
	:	: : : :	:
Qy	196	DKVDESVSTEPISPSWRSEVTFTPALYYTSGTTGLPKAAETHORIWY-GRGLTFVSSL	254
	:	: : : :	:
Db	160	QLKNQ--QPATICYAPPLSTDDBTEILEFTSGTSTRPGKWIVTHYNLRFGAYSAMQCAL	216
	:	: : : :	:
Qy	255	KADVDVITLPFYHSAAALLIGIHCGCIVAGATLALRTRKFSAOFWDCCRKYNNVTVIQICE	314
	:	: : : :	:
Db	217	RDDVDYLTVMPAFHIDCOCTAAMAASAGATFVLVEKYSARAFWQOVQRYRVATECIPM	276
	:	: : : :	:
Qy	315	LLRYLCNSPOKPNDRDHKVR-LALGNGLRGDWVRQFKFRGDCIYEFTAATEGNIGPW-	372
	:	: : : :	:
Db	277	MIRTLMVQPSANDQQRLREVIFYNLNSEQEKDAFCERFG-VRLLTYSGMTTEIVGIIG	335
	:	: : : :	:
Qy	373	---NYARKVGAAGRNVYLQKKIITYDLIKDYDEKDFPVREDENGCYVRVPKGEVGLLVCK-	428
	:	: : : :	:
Db	336	DRPGCDKRBPMSITGRVGC-----YEAS----IRDHNRR--PLPAGEIGEICKG	378

Db 492 NMAKRVPSYLEIR 505

## RESULT 12

hypothetical protein rv1683 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C:Accession: B70501  
R: Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M. A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
A: Authors: Squares, R.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B. G.  
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A: Reference number: A70500; MUID: 98295987  
A: Accession: B70501  
A: Status: preliminary; nucleic acid sequence not shown; translation not shown  
A: Molecule type: DNA  
A: Residues: 1-999 <COL>  
A: Cross-references: GB:Z98268; GB:AL123456; NID: g3261839; PIDN: CAB10940.1; PID: e332852;  
A: Experimental source: strain H37RV  
C: Genetics:  
A: Gene: rv1683

Query Match 11.8%; Score 387.5; DB 2; Length 999;  
Best Local Similarity 25.18; Pred. No. 1e-21;  
Matches 151; Conservative 91; Mismatches 273; Indels 87; Gaps 18;

QY 36 VAAAGRRVRSYQGR-----RPAR-----TIIRAFLEKARQTPHPKFFLLFRDETL 79  
Db 415 VYAAANSRVTLAVETVRLPLRLARLQGLNDHTRISLGRITDEQAHPKFEFLFDGRVH 474  
QY 80 TYAQVDRSNOVARALHDLGROGCVALLMGNEPAYVWLGLVKGCMACLAENYIR 139  
Db 475 TYEAVNRINNVVRL-IAVGROGDRGVLMETRPALVAIAALSRLGAV-----524  
QY 140 AKSLHCFQCCGAKVLLVSPLOAAVE-----EILPSLKKDDVSIIYVSRSTNTDGIDS- 193  
Db 525 -----AVVMRPDITLSASVRLGRVTEILTPTNLDAARQLPGQVILGGESR 572  
QY 194 -----FLDKYDEVSTEPESWRSEVTFPPALYIYTSQTTGLPKAMIT 238  
Db 573 DLDLPADALEOGQVIDMEKIDPDAVE-LPAMYRPNFGLARDLAFIASSADGDLVAKQIT 631  
QY 239 HORIW-----YGTGLTFVSGLKADDDVIITLFPVHSAALLIGIHGCIIVAGATLALTKFSA 294  
Db 632 NYR-WAVSAFCTAALGRR--DTVYCLTPLHESALLVSGVAVGGTRIALSRGLRP 688  
QY 295 SQFDDCKRYNVTYQIGELLRYLCSPOKPNDRDHKVRALGNGLRGDMVRQFVKRF 354  
Db 689 DRFAEVRQYGVTVVYTWAMLRDQVDDPAFVHLGNHPVRLFTGSGMPTGLWERYVEAFA 748  
QY 355 DICIEYFAAPEGNIGFMNYA-RKVGAGRVNYLQKKIITYDLIKYDVEKDEPVRDNGY 413  
Db 749 PAHVVEFATDGAQVLANVAGAKIGSKGRPLPGARV---ELGAYDAEHDLELLENDRG 805  
QY 414 CVRPVKGVEGLLVCKITQLTPFNGYAGAKAQTETKKLRDVRFKGDLDFYNSGDLMLMDHEN 473  
Db 806 VQVAGVQVGVLLAQ--SRGPIDPTASVK-----RGVFAPADTWISTDYLFWRDDG 855  
QY 474 FIYFHDRVGDTRFRKGENVATTEVADTVGLVDFVQEVNRYGVHVPDHEGR-IGMASIKMK 532  
Db 856 DYWLAGRGSVVRARGMVTPEPTNALGLITGVDLAVTYGLV---RGRHVAVSAVTLL 912  
QY 533 ENHEFDGKLFQHIADYLPSPARPRFLRIODTTEITGTGFKHKMTLVEGFNPVAKAL 592  
Db 913 PGATITAADLEAVAS-MPVGLGPDIVHVVPQLTSLGTYRPTVSALRANGI-PKAGROAW 970  
QY 593 YF 594  
Db 971 YF 972

## RESULT 13

probable coA ligase - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 18-Aug-2000  
C:Accession: G70986  
R: Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M. A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
A: Authors: Squares, R.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B. G.  
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A: Reference number: A70500; MUID: 98295987  
A: Accession: G70986  
A: Status: preliminary; nucleic acid sequence not shown; translation not shown  
A: Molecule type: DNA  
A: Residues: 1-532 <COL>  
A: Cross-references: GB:Z95890; GB:AL123456; NID: g3242245; PIDN: CAB09316.1; PID: g21310  
A: Experimental source: strain H37RV  
C: Genetics:  
A: Gene: fadD1  
C: Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology  
F: 48-499/Domain: acetate--CoA ligase homology <ACL>

Query Match 11.8%; Score 385; DB 2; Length 532;  
Best Local Similarity 26.8%; Pred. No. 6.8e-22;  
Matches 142; Conservative 84; Mismatches 209; Indels 94; Gaps 21;

QY 107 VALLMGNEPAYVWLGLVKGCMAC-LNYINIRAKSLHCFQCCGAKVLLVSPLOAAV 165  
Db 55 IGSLLGNTPEML-AQLAAAGLGGVYVLCGLNTRRGDALAADVRADQIVTVDADHALL 113  
QY 166 EELLPSLKKDDVSIIYVSRSTNTDGIDSLDKYDEVSTEPESWRSS-----E 213  
Db 114 -----DGLDLAGARILDTST-----PRNAELVAGDGAFFPYRE 146  
QY 214 VTFTPALYIYTSQTTGLPKAMITH-QRIWYGTGLTFVSGLKADDDVIITLFPVHSAAL 272  
Db 147 VDTMDPFMMIFTSGTSCNPKAVPVSHLMATFAGRSLSRTEQDTCVSPFLHNAV 206  
QY 273 LIGHGCIIVAGATLALTKFSAOFWDDCKRYNVTYQIGELLRYLCSPOKPNDRDHK 332  
Db 207 VAGWAPAVVSGAALAPAT-FSATGFLDDVRRYHATYNYVKGPLAYILATPERDDADNP 265  
QY 333 VRLALGNGLRGDMVRQFVKRGDICIYEFYAATE-----GNIGFMNYARKVG 379  
Db 266 LRVAFGNEANDKDIEEFSSREFG-VQVEDGCGSTENAVIVIREPGTPPGSIG-----RG 317  
QY 380 AVGRVNYLQKKIITYDLIKYDVEKDEPVRDNGYCVRVKGEVGLLVCKITQLTPFNGYA 439  
Db 318 AHGVAVYNGTETVTECAVAREDAHGALTNADE-----AIGELV-NTTSGSFTGY 366  
QY 440 G-AKAQTEKKLRDVRFKKGLDYFNSGDLMLMDHENFIYFHDVRGDTFRKKGENVATTEVA 498  
Db 367 NDPEANER-----MRHGMVW-SGDLAYRSEGWIYLAGRTADMVRVDGENLTAAPIE 418  
QY 499 DTGVLDFVQEVNRYGVHVPD-HEGRIGMASTKMKENHEFDGKLFQHIADYLP---SYA 554  
Db 419 RILLRYKAINRVAVYA--VPDEYVGVQVMAALVLRAGDTFD-PDAFEAFDLAQPDLSKA 475  
QY 555 RPRFLRIODTTEITGTGFKHKMTLVEGFNPVAVIK-DALYFLDDDTAKWY 602  
Db 476 RPRIRIADLPSTATHKVLKROLIDEG--TAVGKADTLWVREPRGSAY 522

## RESULT 14

A69831  
probable acid--CoA ligase (EC 6.2.1.-) yhfL [similarity] - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000

C:Accession: A69831

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
C.: Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall  
iech, J.; Harwood, C.R.; Henaat, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshitawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033

A:Accession: A69831

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-513 &lt;KUN&gt;

A:Cross-references: GB:290109; GB:AL009126; NID:g2633260; PIDN:CABL2867.1; PID:g2633363

A:Experimental source: strain 168

C:Genetics:

C:Gene: yhfL

C:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology

C:Keywords: acid-thiol ligase

F:47-507/Domain: acetate--CoA ligase homology &lt;ACL&gt;

Query Match 10.8%; Score 354.5; DB 2; Length 513;

Best Local Similarity 23.6%; Pred. No. 1.5e-19;

Matches 127; Conservative 95; Mismatches 256; Indels 61; Gaps 15;

QY 61 EKARQPHKFFLLFRDETLYTAQVDRSRNOVARALHDHGLRGQDCVALLMGNEPAYVWL 120

Db 9 ETASEKPDSTACRQDHMTYLLQIYQIFADGLQE-AGMEKGDHALLGLNGLSPDFFITA 67

QY 121 WLGLVKLGCCAMACINYNIRAKSLHLCFQCCGAKVLLVSPLOAABEILPSSKKDDVSYT 180

Db 68 FFGALKAGIVVVPINPLYTPTTEIGYMLTNGDVKAIVGVSQLLPLYESMSHSLPKVELVL 127

QY 181 YVSTSTNTDID-----SFLDKVDEVT-----EPIPEWRSEVTSTPALYITSG 227

Db 128 CQTGEARPEADPEVRMKMTTFKILRPTSAKQONQEPVDD-----TAVILYITSG 178

QY 228 TTGLPKAMITHORIWYGTG-LTFVSGLKADDDVYITLTPYHSAALLIGHGICVAGATL 286

Db 179 TTGPKCAMITHQNLVSNANDVAGYLGMDERDNNVCALPCHVFCLTVCNMNAPLMSGAIV 238

QY 287 ALRTKFSASQFWDCCRYKYNVTIOYIGELLYRLCNQPKQNDNRDHRKVRALGNLGRDV- 345

Db 239 LIEPQFSPASVFKLVKQOQATIFAGVPTMYNLYLFHENGKKDDFSSIRLCISGGASMPVA 298

QY 346 -WROFVKRFQDICIYEFAATEG-IGFMNVARVKGAVG-RVNYLQKKIITYDLIKY 399

Db 299 LLTAFEKFG-VTLEIGYGEASEPVTCFNPFDGRKPGSIGISILHVENKVV----- 350

QY 400 DVEKDEPVRDENGCVRPKGEVLCKITQTLTPFNGYAGAKAQTEKKLRDVFKKGDL 459

Db 351 -----DPLGRE-----LPAHQVGEILVGPV--MKGYKMPMETE-----HALKDGWL 392

QY 460 YFNSGDLMLVDHNFIFTHDRVGTDFRWKGENVATTEVATVGLVDFVQEVNVGVHVPD 519

Db 393 Y--TGDARREDGDFYIVDRKKDMITVGGVNVPREVEVLYSHPDVKEAVIG--VPD 448

QY 520 HEGRIGMASIKMKENHEFDGKKLFOHLADYLPVSRPFRFLRIQDTIEITGTFKHKMTL 578

Db 449 PQSEANVGVVPRSGVTEEDIMQHCCKHLAKYKRAATFELDDIPKNTATKMLREAL 507

RESULT 15

Db2824

regulator of pathogenicity factors XF0287 [imported] - Xylella fastidiosa (strain 9a5  
C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 03-Nov-2000

C:Accession: D82824

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82824

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-569 &lt;SIM&gt;

A:Cross-references: GB:AE003883; GB:AE003849; NID:g9105115; PIDN:AAF83100.1; GSPDB:GN

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv

M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

C:Gene: XF0287

C:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology

F:72-554/Domain: acetate--CoA ligase homology &lt;ACL&gt;

Query Match 10.2%; Score 335; DB 2; Length 569;

Best Local Similarity 24.4%; Pred. No. 5.6e-18;

Matches 139; Conservative 92; Mismatches 243; Indels 96; Gaps 20;

QY 53 RTILRAFLEKARQPHKFFLLFRDETLYTAQVDRSRNOVARALHDHGLRGQDCVALLMG 112

Db 25 RTIADVFTSVIKYRCHPAYTNFGKTLTYGEVLLTKQFASVLLNVLKKGDRALMML 84

QY 113 NEPAVYVWLGLVKLGCCAMACINYNIRAKSLHLCFQCCGAKVLLVSPLOAABEILP 172

Db 85 NCLQTPVATFGALCAGLVVNVNPLYTARELKHQVLDAGSVLVVMDNFTVQIIA-- 142

QY 173 KKDDVSIYVTSNTDIDGID----SFLDKVDEVTPEIPE-----SWRSEVTF--S 217

Db 143 ---DTPIKQVITTELGLDLPKRSINFAVKHKKLVPEYQLPRSFREALALGSKHS 199

QY 218 TPALYI-----YTSGTGLPKAAMITHQRI-----WVGTLTFVSGLKADDV 259

Db 200 MPPIHASSDLAFLQYGTGTGTPKGAMLTHRNVMVANNQVQSQMLQTSNLSKEG--ET 256

QY 260 IVITLPPVHSAAL-----LIGHGC--IVAGATIALRTKFSASQFWDCCRYKYNVTIOY 311

Db 257 VLTALPLHIFALTANSLVFMKIGCNHLISNPR-NMRT-----FVKELQVRFTVITG 309

QY 312 IGELLYRLCNQPKQNDNRDHRKVRALGNL-----RGDWRQFVKRFQDICIYEFAATE 366

Db 310 VNTFLKLNLTGPFKDLFSSLLKIALGGWVIQSRVABQKQV-----HVPFLIEAYGUTE 365

QY 367 GN-----IGFMNVARVKGAVGRVNYLQKKIITYDLIKYDVEKDEPVRDENGCVRPKGEV 422

Db 366 ASPEACINPLNLOEINGSIG-----MFIPTDVC-----IKDNTN--TALPIGEM 408

QY 423 GLLVCKITQTLTPFNGYAGAKAQTEKKLRDVKFGDLTFNSGDLMLVDHNFIFTHDRVG 482

Db 409 GELCIKGPQV--MKGYWQRPEETSE-----VLDADGWLHTGDIYVKMDQKGFXYIIDRKK 460

QY 483 DTFRWKGENVATTEVATVGLVDFVQEVNVGVHVPDHEGRIGMASIKMKENHEFDGKKL 542



Mon Jul 16 18:57:59 2001

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Page 9

Db 461 EIIIVSGFNVPKEIEIEVIAIPGVAEVAAG--VPDEQSGEVVKVIVKKDPMLTAEV 518

QY 543 FQHIADYLPSPYARPRFLRIQDTIEITGTFK 572

Db 519 KAAATNLTRYKLPRIIEFRATLPKTDVGK 548

Search completed: July 16, 2001, 18:13:54  
Job time: 155 sec

